

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____

Source: _____

Date Processed by STIC: _____

10/578,839

TFWP

05/22/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/578,839

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 05/22/2006

PATENT APPLICATION: US/10/578,839

TIME: 14:20:55

Input Set : A:\Q94769 sequence listing.txt

Output Set: N:\CRF4\05222006\J578839.raw

3 <110> APPLICANT: INJE UNIVERSITY
 5 <120> TITLE OF INVENTION: CANCER CELL TARGETING GENE DELIVERY METHOD
 7 <130> FILE REFERENCE: Q94769
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/578,839
 C--> 9 <141> CURRENT FILING DATE: 2006-05-10
 9 <150> PRIOR APPLICATION NUMBER: KR 10-2003-0079897
 10 <151> PRIOR FILING DATE: 1003-11-12
 12 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/000545
 13 <151> PRIOR FILING DATE: 2004-03-15
 15 <160> NUMBER OF SEQ ID NOS: 11
 17 <170> SOFTWARE: KopatentIn 1.71
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 36
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Env F primer
 28 <400> SEQUENCE: 1
 29
 cgcggtatccg aattccatac ctggtgttgc tgacta
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 47
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: 597LN primer
 41 <400> SEQUENCE: 2
 42
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 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 49
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: LC597 primer
 54 <400> SEQUENCE: 3
 55
 caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 35
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:
 64 <223> OTHER INFORMATION: Spike R2 primer

Does Not Comply
Corrected Diskette Needed

Cpg -1,3,4-11)
wrapped
Sequences.
Pls See pg-3

67 <400> SEQUENCE: 4

68

tgctctagaa ttcttaaagg ttaccttcgt tctct

35

<110> APPLICANT: INJE UNIVERSITY
<120> TITLE OF INVENTION: CANCER CELL TARGETING GENE DELIVERY METHOD
<130> FILE REFERENCE: Q94769
<140> CURRENT APPLICATION NUMBER: US/10/578,839
<141> CURRENT FILING DATE: 2006-05-10
<150> PRIOR APPLICATION NUMBER: KR 10-2003-0079897
<151> PRIOR FILING DATE: 1003-11-12
<150> PRIOR APPLICATION NUMBER: PCT/KR2004/000545
<151> PRIOR FILING DATE: 2004-03-15
<160> NUMBER OF SEQ ID NOS: 11
<170> SOFTWARE: KopatentIn 1.71

<210> SEQ ID NO 1
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Env F primer
<400> SEQUENCE: 1
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36

The number is wrapped down to the next line. Pls see item 1 on Error Summary sheet.

<210> SEQ ID NO 2
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 597LN primer
<400> SEQUENCE: 2
agctggacct ggctgccacc acctccgcta ttttggtccc attttac
47

Same error

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

<210> 8
<211> 786
<212> DNA
<213> Tag-72pS1

Invalid Response. 2137 Responses
can be either Artificial, Unknown
or Genus Species. Pls see
Item 10 on Error Summary
Sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/578,839

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Input Set : A:\Q94769 sequence listing.txt
Output Set: N:\CRF4\05222006\J578839.raw

71 <210> SEQ ID NO: 5
72 <211> LENGTH: 36
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: LnkNScFv primer
80 <400> SEQUENCE: 5
81
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84 <210> SEQ ID NO: 6
85 <211> LENGTH: 36
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: ScFvLnkC primer
93 <400> SEQUENCE: 6
94
actgcctcct ccacctgcgg cgggggttgaa gtccca 36
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 2058
99 <212> TYPE: DNA
100 <213> ORGANISM: SEATO type of GalV Env glycoprotein
102 <220> FEATURE:
103 <221> NAME/KEY: sig_peptide
104 <222> LOCATION: (1)..(126)
106 <220> FEATURE:
107 <221> NAME/KEY: misc_feature
108 <222> LOCATION: (127)..(1467)
109 <223> OTHER INFORMATION: surface subunit region
112 <220> FEATURE:
113 <221> NAME/KEY: misc_feature
114 <222> LOCATION: (1468)..(2025)
115 <223> OTHER INFORMATION: transmembrain domain
118 <400> SEQUENCE: 7
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121
atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc 120
123
gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180
125
tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
127
cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300
129
ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360
131
tataagcaaa tcacctgggg agccataggg tgcagctacc ctcggttag gactagaatg 420
133
gcaagctcta cttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480
135
tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
137

Same Error

*wrappe
Sequence*

tattggctat	ctaaatcctc	aaaagacctc	ataactgtaa	aatgggacca	aaatagcgaa	600
139						
tggactcaaa	aatttcaaca	gtgtcaccag	accggctggg	gtaacccccct	taaaatagat	660
141						
ttcacagaca	aaggaaaatt	atccaaggac	tgataaacgg	gaaaaacctg	gggattaaga	720
143						
ttctatgtgt	ctggacatcc	aggcgtacag	ttcaccattc	gcttaaaaat	caccaacatg	780
145						
ccagctgtgg	cagtaggtcc	tgacctcgtc	cttgtggaac	aaggacctcc	tagaacgtcc	840
147						
ctcgtctctc	cacctcctct	tcccccaagg	gaagcgccac	cgccatctct	ccccgactct	900
149						
aactccacag	ccctggcgac	tagtgacaaa	actcccacgg	tgagaaaaac	aattgttacc	960
151						
ctaaacactc	cgctccccc	cacaggcgac	agactttttg	atcttgtgca	gggggccttc	1020

Same Error

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DATE: 05/22/2006

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Input Set : A:\Q94769 sequence listing.txt

Output Set: N:\CRF4\05222006\J578839.raw

153
: ctaaccttaa atgctaccaa cccagggggcc actgagtctt gctggctttg tttggccatg 1080
155
ggccccctt attatgaagc aatagcctca tcaggagagg tgcctactc caccgacctt 1140
157
gaccggtgcc gctggggggac ccaaggaaag ctcacctca ctgaggtctc aggacacggg 1200
159
ttgtgcatag gaaagggtgcc ctttaccat cagcatctct gcaatcagac cctatccatc 1260
161
aattcctccg gagaccatca gtatctgtc cctccaacc atagctggtg ggcttgacgc 1320
163
actggcctca ccccttgcc ctccacctca gtttttaatc agactagaga tttctgtatc 1380
165
caggctccagc tgattcctcg catctattac taccctgaag aagttttgtt acaggcctat 1440
167
gacaattctc accccaggac taaaagagag gctgtctcac ttaccctagc tgttttactg 1500
169
gggttgggaa tcacggcggg aatagggtact ggttcaactg ccttaattaa aggacctata 1560
171
gacctccagc aaggcctgac aagcctccag atcgccatag atgctgacct ccgggcccctc 1620
173
caagactcag tcagcaagtt agaggactca ctgacttccc tgtccgaggt agtgcctcaa 1680
175
aataggagag gccttgactt gctgtttcta aaagaagggtg gcctctgtgc ggccctaaag 1740
177
gaagagtgtt gtttttacat agaccactca ggtgcagtac gggactccat gaaaaaactc 1800
179
aaagaaaaaac tggataaaag acagttagag cgccagaaaa gccaaaactg gtatgaagga 1860
181
tggttcaata actccccttg gttcactacc ctgctatcaa ccacgctgg gccctatta 1920
183
ctctccttc tgttgctcat cctcgggcca tgcacatca ataagttagt tcaattcatc 1980
185
aatgatagga taagtgcagt taaaattctg gtccttagac aaaaatatca ggccctagag 2040
187
aacgaaggta acctttaa 2058

190 <210> SEQ ID NO: 8
191 <211> LENGTH: 786
192 <212> TYPE: DNA
193 <213> ORGANISM: Tag-72pS1
195 <220> FEATURE:
196 <221> NAME/KEY: misc_feature
197 <222> LOCATION: (346)..(390)
198 <223> OTHER INFORMATION: (Gly4Ser)3 linker
201 <220> FEATURE:
202 <221> NAME/KEY: misc_feature
203 <222> LOCATION: (739)..(777)
204 <223> OTHER INFORMATION: PreS1 Tag
207 <400> SEQUENCE: 8
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210
tcctgcaagg cttctggcta caccttcact gaccatgcaa ttcactgggt gcgccaggcc 120

Sequence

212
cctggacaac gccttgagtg gatgggatat ttttctcctg gcaacgatga ttttaaatac 180
214
tcccagaagt tccagggacg cgtgacaatc actgcagaca aatccgcgag cacagcctac 240
216
atggagctga gcagcctgag atctgaggac acggcggtct attactgtgc aagatcggtg 300
218
aacatggcat actggggcca agggactctg gtcactgtct cttcaggtgg aggcgggttca 360
220
ggcgagggtg gctctggcgg tggcggatcg gacattgtga tgaccagtc tccagactcc 420
222
ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgtttta 480
224
tacagcagac acaataagaa ctacttagct tgggtaccagc agaaaccagg acagcctcct 540
226
aagctgctca tttactgggc atctaccggg gaatccgggg tccctgaccg attcagtggc 600
228
agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660
230
gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaaggtg 720
232
gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc 780
234
gcatag 786
237 <210> SEQ ID NO: 9
238 <211> LENGTH: 13
239 <212> TYPE: PRT
240 <213> ORGANISM: PreS1 epitope at C-terminal of Tag-72pS1

Same
Error

RAW SEQUENCE LISTING

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DATE: 05/22/2006

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Input Set : A:\Q94769 sequence listing.txt

Output Set: N:\CRF4\05222006\J578839.raw

242 <400> SEQUENCE: 9

243 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro

244 1 5 10

247 <210> SEQ ID NO: 10

248 <211> LENGTH: 2871

249 <212> TYPE: DNA

250 <213> ORGANISM: Artificial Sequence

252 <220> FEATURE:

253 <223> OTHER INFORMATION: ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

256 <400> SEQUENCE: 10

257

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259	
atgagtctctg ggagctggaa aagactgata atcctcttaa gctgcgtatt cggcggcggc	120
261	
gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg	180
263	
tcccaaaactg gagacgttgt ctgggataca aaggcagtcc agcccccttg gacttggtgg	240
265	
cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg	300
267	
ggaaccgatg tctcgtcttc taaacgagtc agacctccgg actcagacta tactgccgct	360
269	
tataagcaaa tcacctgggg agccataggg tgcagctacc ctggggctag gactagaatg	420
271	
gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg	480
273	
tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt	540
275	
tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgga	600
277	
ggtggtggca gccaggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct	660
279	
tcagtgaagg tgcctgcaa ggcttctggc tacaccttca ctgacctgac aattcactgg	720
281	
gtgcgccagg cccctggaca acgccttgag tggatgggat atttttctcc tggcaacgat	780
283	
gattttaaat actcccagaa gttccaggga cgcgtgacaa tcaactgcaga caaatccgcg	840
285	
agcacagcct acatggagct gagcagcctg agatctgagg acacggcggc ctattactgt	900
287	
gcaagatcgt tgaacatggc atactggggc caagggactc tggtcactgt ctcttcaggt	960
289	
ggaggcgggt caggcggagg tggctctggc ggtggcggat cggacattgt gatgaccag	1020
291	
tctccagact ccctggctgt gtctctgggc gagagggcca ccatcaactg caagtccagc	1080
293	
cagagtgttt tatacagcag caacaataag aactacttag cttggtacca gcagaaacca	1140
295	
ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac	1200
297	
cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag cctgcaggct	1260
299	

same
ever

gaagatgtgg cagtttatta ctgtcagcaa tattattcct atccgttgac gtteggccaa 301	1320
gggaccaagg tggaaatcaa agcggccgca ggagccaacg caaacaatcc agattgggac 303	1380
ttcaaccccg ccgcaggtgg aggaggcagt gaatggactc aaaaatttca acagtgtcac 305	1440
cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag 307	1500
gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta 309	1560
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gtccttgtgg aacaaggacc tcctagaacg tccctcgtc tcccacctcc tcttccccca 313	1680
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caaactccca cggtgagaaa aacaattggt accctaaaca ctccgcctcc caccacaggc 317	1800
gacagacttt ttgatcttgt gcagggggcc ttcctaacct taaatgctac caaccaggg 319	1860
gccactgagt cttgctggct ttgtttggcc atgggcccc cttattatga agcaatagcc 321	1920
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aagctcacc tcaactgaggt ctcaggacac gggttgtgca taggaaagggt gccctttacc 325	2040
catcagcatc tctgcaatca gacctatcc atcaattcct ccggagacca tcagtatctg 327	2100
ctcccccca accatagctg gtgggcttgc agcactggcc tcacctcttg cctctccacc 329	2160
tcagttttta atcagactag agatttctgt atccaggctc agctgattcc tcgcatctat 331	2220
tactatcctg aagaagtttt gttacaggcc tatgacaatt ctcacccag gactaaaaga 333	2280
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*Same
Error*

RAW SEQUENCE LISTING

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Input Set : A:\Q94769 sequence listing.txt

Output Set: N:\CRF4\05222006\J578839.raw

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337
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339
tcactgactt cctgtccga ggtagtgtc caaatagga gaggccttga cttgctgttt 2520
341
ctaaaagaag gtggcctctg tgcggcccta aaggaagagt gctgttttta catagaccac 2580
343
tcaggtgcag tacgggactc catgaaaaaa ctcaaagaaa aactggataa aagacagta 2640
345
gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcact 2700
347
accctgctat caaccatcgc tgggccccta ttactcctcc ttctgttgct catcctcggg 2760
349
ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
351
ctgggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871

354 <210> SEQ ID NO: 11
355 <211> LENGTH: 956
356 <212> TYPE: PRT
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: ScFv-GaLV Env GP chimeric ligand (FvGEL199)
363 <400> SEQUENCE: 11

364 Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
365 1 5 10 15
367 Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
368 20 25 30
370 Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
371 35 40 45
373 Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
374 50 55 60
376 Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
377 65 70 75 80
379 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
380 85 90 95
382 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Lys Arg Val Arg Pro
383 100 105 110
385 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
386 115 120 125
388 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
389 130 135 140
391 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
392 145 150 155 160
394 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
395 165 170 175
397 Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
398 180 185 190
400 Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Ser Gln Val Gln Leu
401 195 200 205
403 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
404 210 215 220

same
error

406 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
407 225 230 235 240
409 Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
410 245 250 255
412 Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/578,839

DATE: 05/22/2006

TIME: 14:20:56

Input Set : A:\Q94769 sequence listing.txt

Output Set: N:\CRF4\05222006\J578839.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date